ANTIBIOTIC SUSCEPTIBILITY PATTERN AND PHENOTYPIC CHARACTERIZATION OF EXTENDED-SPECTRUM-BETA-LACTAMASE-PRODUCING Enterobacteriaceae ISOLATED FROM VARIOUS CLINICAL SAMPLES

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Abstract

The spread of antibiotic resistant organisms and those producing extended spectrum β-lactamases (ESBL) has become a health care problem worldwide in communities and hospitals, as it leads to more complicated infections, longer duration of treatment, and increases in patient mortality. In the present study, we analyzed 226 clinical samples in order to assess the spread of ESBL-producing Enterobacteriaceae. 196 Enterobacteriaceae were identified and classified as members of the genera Pantoea, Klebsiella, Escherichia, Enterobacter, Serratia, Proteus, Citrobacter, and Raoultella. The results of susceptibility testing of isolated strains to 19 antibiotics showed that the most part of the isolates were highly resistant (p<0.01) to the tested β-lactams: penicillins and penicillin like antibiotics (amoxicillin, ticarcillin and amoxicillin-clavulanic acid), first-generation cephalosporins (cephalexin), and second generation cephalosporins (cefoxin), and second generation cephalosporins (cefoxitin). 60.20% of the Enterobacteriaceae isolates were multi-drug resistant (MDR) strains. Resistant isolates to third generation cephalosporins were tested for ESBL by tree methods, concluding its presence in 29.59% of the isolates by double-disk synergy test, 27.55% by the disk approximation method and by 31.63% double-disk test. High levels of MDR strains and ESBL-producing Enterobacteriaceae in our study suggest the need for applying specific infection control measures, and rational antibiotic use to reduce the selection pressure and prevent dissemination of resistant bacteria.

Keywords: antimicrobial susceptibility, clinical samples, Enterobacteriaceae, extended-spectrum β-lactamases (ESBL)-producing and multi-drug resistance.

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